REMARKS

In view of the above amendments and the following remarks, reconsideration of the outstanding office action is respectfully requested. Pursuant to 37 CFR § 1.21, attached as an Appendix is a Version With Markings to Show Changes Made.

The objection to claim 19 under 37 C.F.R. § 1.75(c) is respectfully traversed in view of the above amendments.

The objection to claims 2-20, 23-26, 28-29, 31, 33-43, 46-57, 59-81, and 93-94 is respectfully traversed in view of the above amendments.

The rejection of claims 1-20, 23-29, 31-43, 46-81, and 93-94 under 35 U.S.C. § 112 (1st para.) for failure to satisfy the written description requirement is respectfully traversed.

The examples of the present application describe the preparation of constructs involving the fusion of various N gene fragments from tomato spotted wilt virus to the gene encoding a green fluorescent protein or the gene encoding the turnip mosaic potyvirus coat protein gene and transformation of plants with the resulting chimeric gene. The transgenic plants are resistant to the tomato spotted wilt virus even if the N gene fragment is not of sufficient length to independently impart virus resistance to that plant.

The present application also teaches that the subject matter of the present application can be used to couple a silencer DNA molecule to fragments of different coat protein encoding genes from different strains of papaya ringspot virus in order to produce a transgenic papaya that is resistant to all papaya ringspot virus strains. See page 11, line 33 to page 12, line 15 of the present application.

Another aspect of the present invention is to impart to a plant resistance to a plurality of different viruses. For example, a transgenic potato can be made resistance to potato leafroll virus, potato virus Y, and potato virus X by transforming a potato with fragments of the coat protein encoding gene from each of these viruses in a single transformation event. See page 12, lines 16-34 of the present application.

A further embodiment of the present invention is set forth on page 13, lines 1-12 of the present application which describes imparting resistance to squash by forming a construct containing fragments from the coat protein genes of zucchini yellow mosaic virus,

papaya ringspot virus, watermelon mosaic virus II, and squash mosaic virus and transforming them into squash.

With this information, one of ordinary skill in the art would have been able to prepare these and other transgenic plants containing trait DNA molecule(s) fused to silencer DNA molecules in accordance with the present invention.

The outstanding office action criticizes the disclosure of the present application for failing to disclose DNA sequences for nucleic acid molecules used to transform plants in accordance with the present invention. However, the subject matter of the present application does not involve the discovery of new naturally-existing DNA molecules. It, instead, involves the use of known sequence information to impart various traits (including virus resistance) to plants by using one or more fragments of those sequences (at least one of which has a length insufficient to impart that trait). Since the naturally-existing DNA molecules are known, one of ordinary skill in the art would be fully able to adapt that information to practice the present information as described above.

For all of these reasons, the rejection of claims 1-20, 23-29, 31-43, 46-81, and 93-94 under 35 U.S.C. § 112 (1st para.) for failure to satisfy the written description requirement should be withdrawn.

The rejection of claims 1-20, 23-29, 31-43, 46-81, and 93-94 under 35 U.S.C. § 112 (1st para.) for failure to satisfy the written description requirement is respectfully traversed.

In the outstanding office action, it is asserted that support in the present application is lacking for the phrases "wherein said trait DNA molecule and said silencer DNA molecule are heterologous to one another" and "wherein at least one of said trait DNA molecule or said silencer DNA molecule is not endogenous to a plant".

The latter phrase has been revised by the above amendments to be "wherein said trait DNA molecule and said silencer DNA molecule are heterologous to plants". Support for this limitation is found on page 17, lines 7-10 and page 18, lines 25-26 of the present application. The term "heterologous" is defined as "not normally present" on page 19, lines 31 of the present application. In addition, the examples of the present application teach the use of a N capsid protein encoding gene from tomato spotted wilt virus as a trait DNA molecule and a DNA molecule encoding a jellyfish green fluorescent protein or a turnip

mosaic potyvirus coat protein as a silencer DNA molecule (see Examples 6-7). Clearly, these genes are not naturally found in plants and, therefore, are heterologous to plants.

As to the phrase "wherein said trait DNA molecule and said silencer DNA molecule are heterologous to one another", applicants respectfully disagree with any suggestion that the requirements of 35 U.S.C. § 112 (1st para.) are not satisfied. Even if the precise words in this quote are not found in the present application, the first paragraph of Section 112 do not describe *ipsimis verbis* support to be satisfied. See Ralston Purina Co. v. Far-Mar Co., 772 F.2d 1570, 227 USPQ 177 (Fed. Cir. 1985). Here, the examples of the present application teach the use of a N capsid protein encoding gene from tomato spotted wilt virus as a trait DNA molecule and a DNA molecule encoding a jellyfish green fluorescent protein or a turnip mosaic potyvirus coat protein as a silencer DNA molecule (see Examples 6-7). In particular, after disclosing the use of various forms of the N protein encoding gene from tomato spotted wilt virus, it is noted on page 38, lines 18-20 and page 45, lines 19-24 that such viral genes can be fused with a non-viral green fluorescent protein sequence. Since these genes are from different sources, applicants submit that the above-quoted language is fully supported by the specification of the present application.

Accordingly, the rejection under 35 U.S.C. § 112 (1st para.) should be withdrawn.

The rejection of claims 1-20, 23-29, 31-43, 46-81, and 93-94 under 35 U.S.C. § 112 (1st para.) for lack of enablement is respectfully traversed for substantially the reasons noted above with regard to the rejection of claims 1-20, 23-29, 31-43, 46-81, and 93-94 under 35 U.S.C. § 112 (1st para.) for failure to satisfy the written description requirement.

It is noted in the outstanding office action that enablement is lacking, because no minimum lengths of the trait DNA molecule and silencer DNA molecule are disclosed. Applicants respectfully disagree. Examples 1-5 of the present application teach how to prepare constructs containing different lengths of the tomato spotted wilt virus N gene and determining whether the resulting plants are resistant or susceptible to that virus. One of ordinary skill in the art is highly educated and experienced in producing transgenic plants, such as transgenic plants which are resistant to plant viruses as a result of the incorporation of genes from viral pathogens in these plants. Those individuals would be fully able to carry out the method of the present invention by routine experimentation (i.e. preparing constructs incorporating trait DNA molecules (having a length that is insufficient to impart that trait to

plants) and silencer DNA molecules, transforming that construct into plants, and determining whether the resulting plants possess the desired trait). What the present application teaches is that it is possible to impart a trait to plants by transforming them with a trait DNA molecule, which has a length insufficient to independently impart the trait to a plant, coupled to a silencer DNA molecule. With applicants' discovery, one of ordinary skill in the art would be fully able to practice the present invention with a wide variety of trait DNA and silencer DNA molecules through routine experimentation.

For all of these reasons, the rejection of claims 1-20, 23-29, 31-43, 46-81, and 93-94 under 35 U.S.C. § 112 (1st para.) for lack of enablement should be withdrawn.

The rejection of claims 1-20, 23-29, 31-43, 46-81, and 93-94 under 35 U.S.C. § 112 (2nd para.) for indefiniteness is respectfully traversed, except as noted below, in view of the above amendments.

The view that the terms "trait DNA molecule" and "silencer DNA molecule" create indefiniteness is incorrect. As clearly stated in claim 1, the trait DNA molecule has a length that is insufficient to independently impart a desired trait to plants transformed with said trait DNA molecule, while the silencer DNA molecule is effective to achieve post-transcriptional gene silencing. The mere fact that the silencer DNA molecule may (or may not) encode a protein does not preclude it from being a silencer DNA molecule as long as it effects post-transcriptional gene silencing. The phrase post-transcriptional gene silencing is fully explained on page 6, line 5 to page 10, line 13 and page 18, line 32 to page 19, line 3 of the present application and, therefore, does not render the claims indefinite.

Accordingly, the rejection under 35 U.S.C. § 112 (2nd para.) is improper and should be withdrawn.

The rejection of claims 1-2, 6-9, 13-16, 18-20, 23-24, 26-29, 31-33, 37-40, 42-43, 46-47, 51-53, 55-59, 63-65, 68-71, 75-76, 80-81, and 93-94 under 35 U.S.C. § 102(b) as anticipated by Seymour, et. al., "Down-Regulation of Two Non-Homologous Endogenous Tomato Genes With a Single Chimeric Sense Gene Construct," Plant Molecular Biology 23: 1-9 (1993)("Seymour") is respectfully traversed.

Seymour transforms tomato with a gene construct which includes a gene having 1320 base pairs and encoding the full length pectinesterase ("PE") enzyme fused to a 244 base pair gene fragment encoding the N-terminus of the polygalacturonase ("PG") enzyme. The construct ("PGPE") is positioned between the CaMV 35S promoter and

terminator. When this construct was transformed into tomato, it was found that expression of the endogenous tomato PG and PE genes, as well as the PGPE gene, were inhibited in the tomato fruit. Since Seymour transforms tomato with 2 genes endogenous to tomato, it cannot satisfy the "wherein said trait DNA molecule and said silencer DNA molecule are heterologous to plants" limitation. Accordingly, Seymour cannot anticipate the pending claims, and, therefore, the rejection under 35 U.S.C. § 102 which is based on that reference should be withdrawn.

The rejection of claims 1-5, 8-12, 15-17, 19-20, 23-25, 27-29, 31-36, 39-41, 43, 46-50, 53-54, 56-57, and 93-94 under 35 U.S.C. § 102(b) as anticipated by Lawson, et. al., "Engineering Resistance to Mixed Virus Infection in a Commercial Potato Cultivar: Resistance to Potato Virus X and Potato Virus Y in Transgenic Russet Burbank," Bio/Technol. 8: 127-34 (1990)("Lawson") is respectfully traversed.

Lawson discloses a DNA construct having a full-length cDNA coat protein of each of potato virus X ("PVX") and potato virus Y ("PVY"), and a method of conferring resistance to infection by PVX and PVY in potato plants transformed with such a construct. However, the coat protein genes used by Lawson are alone sufficient to impart resistance to PVY or PVX, respectively (see page 130, paragraph bridging columns 1 and 2 and the first full paragraph of column 2). In addition, when the coat protein encoding genes are put in the same expression vector, they each have their own separate promoter (see Figure 2). Thus, Lawson does not teach "a trait DNA molecule which has a length that is insufficient to independently impart a desired trait to plants transformed with said trait DNA molecule", nor "a single promoter sequence which effects transcription of both the trait DNA molecule and the silencer DNA molecule", as claimed. Accordingly, this reference cannot be properly used to reject the claims and the anticipation rejection based on it should be withdrawn.

The rejection of claims 1-5, 8-12, 15-17, 19-20, 23-25, 27-29, 31-36, 39-41, 43, 46-50, 53-54, 56-62, 65-67, 69-74, 77-78, 80-81, and 93-94 under 35 U.S.C. § 102(a) as anticipated by WO 96/21031 to Tricoli, et. al., ("Tricoli") is respectfully traversed.

Tricoli teaches a chimeric recombinant DNA molecule having a plurality of DNA sequences, each DNA sequence having a plant-functional promoter linked to a coding region which encodes a virus-associated coat protein. Thus, Tricoli does not teach "a single promoter sequence which effects transcription of both the trait DNA molecule and the

silencer DNA molecule", as claimed. Accordingly, this reference cannot be properly used to reject the claims and the anticipation rejection based on it should be withdrawn.

The rejection of claims 1-2, 6-8, 13-15, 17, 19-20, 23-24, 26-29, 31-33, 37-39, 41, 43, 46-47, 51-52, 54, 56-59, 63-65, 67, 69-71, 75-76, 78, 80-81, and 93-94 under 35 U.S.C. § 102(b) as anticipated by Van Blokland, et. al., "Transgene-Mediated Suppression of Chalcone Synthase Expression in *Petunia hybrida* Results from an Increase in RNA Turnover," Plant J. 6: 861-77 (1994)("Van Blokland") taken with Van der Krol, et. al., "Inhibition of Flower Pigmentation by Antisense CHS Genes: Promoter and Minimal Sequence Requirements for the Antisense Effect," Plant Mol. Biol. 14: 457-66 (1990)("Van der Krol") is respectfully traversed.

Van Blokland discloses suppression of pigmentation in petunia plants transformed with a DNA construct containing the ß-glucuronidase gene linked to the full-length pigmentation gene chalcone synthase ("*chs*") gene from petunia, or either the 5' half or the 3' half of that gene.

Van der Krol teaches an antisense gene encoding RNA complementary to the 5' half of the *chs* mRNA does not show phenotypic effects in transgenic petunia plants.

Since both Van Blokland and Van der Krol work with the *chs* gene from petunia, neither of these references can satisfy the "wherein said trait DNA molecule and silencer DNA molecule are heterologous to plants" limitation. Accordingly, the rejection under 35 U.S.C. § 102(b) based on these references should be withdrawn.

In view of all the foregoing, it is submitted that this case is in condition for allowance and such allowance is earnestly solicited.

Respectfully submitted,

Date: October 8, 2002

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In reference to the amendments made to claims 1-5, 9-12, 16-20, 24-25, 28-31, 33-36, 40-43, 46-50, 53-57, 59-62, 66-69, 70-74, 77-81, and 93-94, additions appear as underlined text, while deletions appear as bracketed text, as indicated below:

Please amend claims 1-5, 9-12, 16-20, 24-25, 28-31, 33-36, 40-43, 46-50, 53-57, 59-62, 66-69, 70-74, 77-81, and 93-94 as follows:

1. (Twice Amended) A DNA construct comprising:

[a fusion gene comprising:]

a trait DNA molecule which has a length that is insufficient to independently impart a desired trait to plants transformed with said trait DNA molecule and

a silencer DNA molecule effective to achieve post-transcriptional gene silencing and [operatively] coupled to said trait DNA molecule, wherein said trait DNA molecule and silencer DNA molecule are heterologous to each other and collectively impart the trait to plants transformed with said DNA construct and wherein [at least one of] said trait DNA molecule [or] and said silencer DNA molecule [is not endogenous] are heterologous to [a] plants;

a single promoter sequence which effects transcription of both the trait DNA molecule and the silencer DNA molecule; and

a single termination sequence which ends transcription of both the trait DNA molecule and the silencer DNA molecule.

2. (Amended) [A] The DNA construct according to claim 1, wherein said DNA construct comprises a plurality of different trait DNA molecules [each having], at least one of which has a length that is insufficient to impart that different trait to plants transformed with that different trait DNA molecule.

3. (Amended) [A] The DNA construct according to claim 2, wherein at least one of the different trait DNA molecules is a viral cDNA molecule and the trait is viral disease resistance.

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4. (Amended) [A] The DNA construct according to claim 3, wherein said viral cDNA molecule[s are] is selected from the group consisting of a DNA molecule encoding a coat protein, a DNA molecule encoding a replicase, a DNA molecule not encoding a protein, a DNA molecule encoding a viral gene product, and combinations thereof.

5. (Amended) [A] The DNA construct according to claim 3, wherein said viral cDNA molecule is from a plant virus selected from the group consisting of tomato spotted wilt virus, impatiens necrotic spot virus, groundnut ringspot virus, potato virus Y, potato virus X, tobacco mosaic virus, turnip mosaic virus, tobacco etch virus, papaya ringspot virus, tomato mottle virus, and tomato yellow leaf curl virus[, and combinations thereof].

9. (Amended) [A] The DNA construct according to claim 2, wherein said silencer DNA molecule is selected from the group consisting of a viral cDNA molecule, a jellyfish green fluorescence protein encoding DNA molecule, [a plant DNA molecule,]a viral gene silencer, and combinations thereof.

10. (Amended) [A] The DNA construct according to claim 1, wherein the trait DNA molecule is a viral cDNA molecule and the trait is viral disease resistance.

11. (Amended) [A] The DNA construct according to claim 10, wherein said viral cDNA molecule is selected from the group consisting of a DNA molecule encoding a coat protein, a DNA molecule encoding a replicase, a DNA molecule not encoding a protein, a DNA molecule encoding a viral gene product, and combinations thereof.

12. (Amended) [A] The DNA construct according to claim 10, wherein said viral cDNA molecule is from a plant virus selected from the group consisting of tomato spotted wilt virus, impatiens necrotic spot virus, groundnut ringspot virus, potato virus Y, potato virus X, tobacco mosaic virus, turnip mosaic virus, tobacco etch virus, papaya ringspot

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virus[, a DNA molecule not encoding a protein], tomato mottle virus, and tomato yellow leaf curl virus[, and combinations thereof].

16. (Amended) [A] The DNA construct according to claim 1, wherein the silencer DNA molecule is selected from the group consisting of a viral cDNA molecule, a jellyfish green fluorescence protein encoding DNA molecule, [a plant DNA molecule,]a viral gene silencer, and combinations thereof.

17. (Amended) [A] The DNA construct according to claim 1, wherein said trait DNA molecule and said silencer DNA molecule encode RNA molecules which are translatable.

18. (Amended) [A] The DNA construct according to claim 1, wherein said trait DNA molecule and said silencer DNA molecule encode RNA molecules which are non-translatable.

19. (Twice Amended) [A] The DNA construct according to claim [1]2, wherein, of the plurality of different trait DNA molecules, at least one of the different trait DNA molecules is long enough to impart the trait.

20. (Amended) [A] The DNA construct according to claim 1, wherein said construct effects post-transcriptional gene silencing within plants.

24. (Amended) [A] The DNA expression vector according to claim 23, wherein said DNA construct comprises a plurality of different trait DNA molecules [each having], at least one of which has a length that is insufficient to impart the different trait to plants transformed with that different trait DNA molecule.

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25. (Amended) [A] The DNA expression vector according to claim 24, wherein at least one of the different trait DNA molecules is a viral cDNA molecule and the trait is viral disease resistance.

28. (Amended) [A] The host cell according to claim [26] 27, wherein said DNA construct comprises a plurality of different trait DNA molecules [each having], at least one of which has a length that is insufficient to impart the different trait to plants transformed that different trait DNA molecule.

29. (Amended) [A] The host cell according to claim 28, wherein said DNA construct is within an expression vector.

30. (Amended) [A] The host cell according to claim 28, wherein said host cell is bacterial.

31. (Amended) [A] The host cell according to claim 28, wherein said host cell is a plant cell.

33. (Amended) [A] The transgenic plant according to claim 32, wherein said DNA construct comprises a plurality of different trait DNA molecules [each having], at least one of which has a length that is insufficient to impart the different trait to plants transformed with that different trait DNA molecule.

34. (Amended) [A] The transgenic plant according to claim 33, wherein at least one of the different trait DNA molecules is a [plant] viral cDNA molecule and the trait is viral disease resistance.

35. (Amended) [A] The transgenic plant according to claim 34, wherein said viral cDNA molecule[s are] is selected from the group consisting of a DNA molecule encoding a coat protein, a DNA molecule encoding a replicase, a DNA molecule not

encoding a protein, a DNA molecule encoding a viral gene product, and combinations thereof.

36. (Amended) [A] The transgenic plant according to claim 34, wherein said plant viral cDNA molecule is from a virus selected from the group consisting of tomato spotted wilt virus, impatiens necrotic spot virus, groundnut ringspot virus, potato virus Y, potato virus X, tobacco mosaic virus, turnip mosaic virus, tobacco etch virus, papaya ringspot virus[, a DNA molecule not encoding a protein], tomato mottle virus, and tomato yellow leaf curl virus[, and combinations thereof].

40. (Amended) [A] The transgenic plant according to claim 33, wherein the silencer DNA molecule is selected from the group consisting of a viral cDNA molecule, a jellyfish green fluorescence protein encoding DNA molecule, [a plant DNA molecule,]a viral gene silencer, and combinations thereof.

41. (Amended) [A] The transgenic plant according to claim 33, wherein said trait DNA molecule and said silencer DNA molecule encode RNA molecules which are translatable.

42. (Amended) [A] The transgenic plant according to claim 33, wherein said trait DNA molecule and said silencer DNA molecule encode RNA molecules which are non-translatable.

43. (Amended) [A] The transgenic plant according to claim 33, wherein the plant is selected from the group consisting of alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, papaya,

sugarcane, *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

46. (Amended) A method of imparting a trait to a plant[s] comprising:

transforming a plant with a DNA construct according to claim 1 under conditions effective to impart a trait to the plant.

47. (Amended) [A] The method according to claim 46, wherein said DNA construct comprises a plurality of different trait DNA molecules [each having], at least one of which have a length that is insufficient to impart the different trait to plants transformed with that different trait DNA molecule.

48. (Amended) [A] The method according to claim 47, wherein at least one of the different trait DNA molecules is a plant viral cDNA molecule and the trait is [a] viral disease resistance.

49. (Amended) [A] The method according to claim 48, wherein said viral cDNA molecule[s are] is selected from the group consisting of a DNA molecule encoding a coat protein, a DNA molecule encoding a replicase, a DNA molecule not encoding a protein, a DNA molecule encoding a viral gene product, and combinations thereof.

50. (Twice Amended) [A] The method according to claim 48, wherein said plant viral DNA molecule is from a virus selected from the group consisting of tomato spotted wilt virus, impatiens necrotic spot virus, groundnut ringspot virus, potato virus Y, potato virus X, tobacco mosaic virus, turnip mosaic virus, tobacco etch virus[, a DNA molecule not encoding a protein], tomato mottle virus, and tomato yellow leaf curl virus[, and combinations thereof].

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53. (Amended) [A] The method according to claim 47, wherein the silencer DNA molecule is selected from the group consisting of a viral cDNA molecule, a jellyfish green fluorescence protein encoding DNA molecule, [a plant DNA molecule,]and combinations thereof.

54. (Amended) [A] The method according to claim 47, wherein said trait DNA molecule and said silencer DNA molecule encode RNA molecules which are translatable.

55. (Amended) [A] The method according to claim 47, wherein said trait DNA molecule and said silencer DNA molecule encode RNA molecules which are non-translatable.

56. (Amended) [A] The method according to claim 47, wherein the plant is selected from the group consisting of alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, [turnip,] radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, papaya, sugarcane, *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

57. (Amended) [A] The method according to claim 47 further comprising:

propagating progeny of the transgenic plant[s].

59. (Amended) [A] The transgenic plant seed according to claim 58, wherein said DNA construct comprises a plurality of different trait DNA molecules [each having], at least one of which has a length that is insufficient to impart that different trait to plants transformed with that different trait DNA molecule.

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60. (Amended) [A] The transgenic plant seed according to claim 59, wherein at least one of the different trait DNA molecules is a viral cDNA molecule and the trait is viral disease resistance.

61. (Amended) [A] The transgenic plant seed according to claim 60, wherein said viral cDNA molecule is selected from the group consisting of a DNA molecule encoding a coat protein, a DNA molecule encoding a replicase, a DNA molecule that does not encode a protein, a DNA molecule encoding a viral gene product, and combinations thereof.

62. (Twice Amended) [A] The transgenic plant seed according to claim 60, wherein said viral cDNA molecule is from a virus selected from the group consisting of tomato spotted wilt virus, impatiens necrotic spot virus, groundnut ringspot virus, potato virus Y, potato virus X, tobacco mosaic virus, turnip mosaic virus, tobacco etch virus, tomato mottle virus, and tomato yellow leaf curl virus[, and combinations thereof].

66. (Amended) [A] The transgenic plant seed according to claim 59, wherein said silencer DNA molecule is selected from the group consisting of a viral cDNA molecule, a jellyfish green fluorescence protein encoding DNA molecule, and combinations thereof.

67. (Amended) [A] The transgenic plant seed according to claim 60, wherein said viral cDNA molecule and said silencer DNA molecule encode RNA molecules which are translatable.

68. (Amended) [A] The transgenic plant seed according to claim 60, wherein said viral cDNA molecule and said silencer DNA molecule encode RNA molecules which are non-translatable.

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69. (Amended) [A] The transgenic plant seed according to claim 59, wherein the plant seed is [for] from a plant selected from the group consisting of alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, papaya, sugarcane, *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

70. (Amended) A method of imparting a trait to plants comprising:

planting a transgenic plant seed according to claim 58 and

propagating a plant from the planted transgenic plant seed under conditions effective to impart a trait to the plant.

71. (Amended) [A] The method according to claim 70, wherein said DNA construct comprises a plurality of different trait DNA molecules [each having], at least one of which have a length that is insufficient to impart that different trait to plants transformed with that different trait DNA molecule.

72. (Amended) [A] The method according to claim 71, wherein at least one of the different trait DNA molecules is a viral cDNA molecule and the trait is [a] viral disease resistance.

73. (Amended) [A] The method according to claim 72, wherein said viral cDNA molecule is selected from the group consisting of a DNA molecule encoding a coat protein, a DNA molecule encoding a replicase, a DNA molecule which does not encode a protein, a DNA molecule encoding a viral gene product, and combinations thereof.

74. (Twice Amended) [A] The method according to claim 72, wherein said viral cDNA molecule is from a virus selected from the group consisting of tomato

spotted wilt virus, impatiens necrotic spot virus, groundnut ringspot virus, potato virus Y, potato virus X, tobacco mosaic virus, turnip mosaic virus, tobacco etch virus, tomato mottle virus, and tomato yellow leaf curl virus[, and combinations thereof].

77. (Amended) [A] The method according to claim 71, wherein the silencer DNA molecule is selected from the group consisting of a viral cDNA molecule, a jellyfish green fluorescence protein encoding DNA molecule, [a plant DNA molecule,]and combinations thereof.

78. (Amended) [A] The method according to claim 71, wherein said trait DNA molecule and said silencer DNA molecule encode RNA molecules which are translatable.

79. (Amended) [A] The method according to claim 71, wherein said trait DNA molecule and said silencer DNA molecule encode RNA molecules which are non-translatable.

80. (Amended) [A] The method according to claim 71, wherein the plant seed is [for] from a plant selected from the group consisting of alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, papaya, sugarcane, *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

81. (Amended) [A] The method according to claim 71 further comprising:

propagating progeny of the transgenic plant[s].

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93. (Amended) [A] The DNA construct according to claim 1, wherein the trait DNA molecule has a length that is greater than 110 nucleotide bases.

94. (Amended) [A] The DNA construct according to claim 1, wherein the trait DNA molecule has a length that is greater than 60 nucleotide bases.